

# Climate Change and Southern Rust (*Puccinia polysora* Underw.) Infection on Corn Cultivars in Korea

Claudino Ninas Nabais<sup>1</sup>, Soon-Kwon Kim<sup>2</sup>, Nwe Win Win<sup>3</sup>, Dhami Narayanan Bahadul<sup>3</sup>, Abu Hendri Saputra<sup>3</sup>, Mohammad Afhzal Sarwari<sup>3</sup>, Tungalag Munkhbat<sup>3</sup>, Don Ho<sup>3</sup>, Moon Ka Hee<sup>3</sup>

<sup>1</sup> Ministry of Agriculture and Fisheries, St. Nicolau Lobato, Comoro, Democratic Republic of Timor-Leste, Po. Box 408

<sup>2</sup> International Corn Foundation, Dongbok-Jesse Bldg, 5Fl, Mapo-Gu, Seoul, Korea Republic, 121-880

<sup>3</sup> International Agricultural Research Institute (IARI), Kyungpook National University, 1370

Sankyuk-dong, Buk-gu, 702-701, Daegu, Korea Republic

E-mail: claudino\_nabais@yahoo.com

**ABSTRACT.** Southern rust is considered as a tropical disease reducing corn (*Zea mays* L.) production. We found similar symptoms at Kunwi Farm in 2006. We have carried out four sets trials of Silage 1 (69B x P45) and Silage 2 (51B x P45) in Jeju and Kunwi in 2008 and 2009, respectively. Materials of P45, 69B and 51B were obtained from Kyungpook National University (KNU) gene bank to develop resistant inbred lines. We used a possibility random mating to all genotypes. Field experiments were designed in a RCBD with three replications. Important agronomic traits were rated and analyzed with SAS 9.1 program, 2005. In Jeju, Southern rust infection was confirmed with highly significant different ( $P=0.001$ ) for both Silage 1 and Silage 2. The infection was highly positive correlation ( $y=1.565 + 0.708x$ ;  $r^2=0.433$  and  $y=2.468 + 0.483x$ ;  $r^2=0.358$ ) with commercial value for Silage 1 and Silage 2, respectively. In Kunwi, the disease was also confirmed with significant ( $P=0.041$ ) and highly significant ( $P=0.001$ ) different for Silage 1 and Silage 2, respectively. The infections were low ( $y=2.337 + 0.372x$ ;  $r^2=0.202$ ) and highly ( $y=1.596 + 0.517x$ ;  $r^2=0.371$ ) positive correlation for Silage 1 and Silage 2, respectively.

Key words: Southern rust, P45, 69B, 51B, Silage 1 and Silage 2

## Introduction

Over the past thirty years, the annual mean temperature has risen by 0.7 Celsius degrees and by 1.4 Celsius degrees just during winter season in South Korea (Jang *et al.* 2009). As a result, the agriculture cultivation area has been extended northward and the damage by blight and harmful insects during the winter has increased (Kim *et al.* 2008). Reilly (1995) stated that agriculture is inherently sensitive to climate condition and is one of the sectors most vulnerable to the risks and impact of global climate change. In the context of increasing food demands and the possible impact of climate change, crop breeding practice should focus on host tolerance to enhance food production. The tolerance principle is known as a co-survival mechanism regarding invading parasites in the environment. This depends on many quantitative genes to develop horizontal resistance (Kim 2000; Ajala *et al.* 2003). This principle accepts the survival of pathogens with host plant without significantly affect to the crop yield. Johnson (1981) defined durable resistance as the resistance that remains effective while being extensively used in agriculture for long period. On the other hand, Lindhout *et al.* (2007) reported that durable resistance is often quantitative, based on the additive effects of some to general genes, and it is not associated with hypersensitive reactions.

Southern rust or Polysora rust caused by *Puccinia polysora* Underwood was identified in Alabama in 1891 in *Triplacum dactyloides* L. (Underwood 1897). This disease was found in the Corn Belt in 1949 (Ullstrup 1965) and 1958 (Hooker 1985), and in Northern Carolina in 1972 and 1973 (Leonard 1974). In West Africa, it was first reported by Rhind *et al.* in 1952 on corn and caused severe epidemics with major yield losses. Cammack (1959) reported the rust spread in Southeast Asia and neighbouring islands with the exception of Borneo, and the larger group in the West Indies, Africa and the South Indian Ocean. Similar symptoms were also reported by Kim (2009) at breeding nursery in Saree, Aceh Province, Indonesia. The pathogen is asexual and produces uredinia on both leaf surfaces and under husks, releasing urediospores from a single postulate more than two weeks (Renfro 1998).

In Korea, it becomes severe in the wet, somewhat in cooler months. Previous evaluations for thousand temperate and tropical materials tested in Kunwi, Jeju, Ansong and on-farm demonstrations in Cheongju, revealed that there were three distinct levels of host response: highly susceptible, highly resistant and intermediate by using rating scale from 1-9. Our breeding experiences showed that high susceptible lines have lesions on all leaves and often affects to form seeds set. Some lines (normally

tropical) were highly resistant, showing very few lesions and only on the upper surface of lower leaves.

The KNU breeding team found symptoms of rust at Kunwi Farm, North Kyung-sang Province, Korea since summer season 2006 (Figure 1A). The symptoms of the rust appeared on the corn leaves surfaces producing small pustules with yellowish to brownish pedicels. Initially, the unclear symptoms created confusion between Common rust (*Puccinia sorghi*) and Southern rust (*Puccinia polysora*). The two diseases are similar, however, it can be distinguished, as pustules of Polysora rust occur predominantly on the upper leaf surface, whereas pustules of Common rust occur abundantly on both leaf surfaces. It was less interesting for further observation during our breeding process. However, the similar symptoms have repeatedly occurring in our trials and breeding materials.

The team started breeding for tolerant inbred lines year-round to develop rust tolerant genotypes. Intensive breeding and trials were carried out at KNU Farm and KNU greenhouses (KNUGH) in Kunwi, Jeju, Ansong and ICF/Cambodia Research Center in Cambodia. The intensive researches and observations in 2008 have brought us to the clearly identification symptoms of Southern rust. Since that, the disease was considered as a minor disease of corn in Korea (Kim 2010 personal communication). We found severe infection of this disease in Jeju Island in 2008 and Kunwi in the mainland, North Gyeongsang Province in 2009. Climate change appears to be the key contributions to this disease infection. This disease is a tropical disease that has been reported by many corn breeders.

## Materials and Methodology

Inbred lines for Silage 1 (69B x P45) and Silage 2 (51B x P45) were obtained from KNU Gene Bank. Materials were developed at KNU GH, Kunwi GH, KNU Farm and ICF/Cambodia Research Center by using recurrent selection to find segregated lines for Southern rust resistance. The breeding team then developed approximately 200 selfings each of 69B, 51B and P45 inbred lines in Kunwi, 2006. Number of lines was increased by selfing continuously to fix the genetic background. The new lines were then developed and screened year-round to obtain favorable alleles for particular quantitatively inherited characters for tolerant to Southern rust and lodging with high grain yield potential.

By repeating cycles of selection, we identified 50 superior segregation lines. The improvement of segregated lines were continued to find additive gene action by random

mating with similar flowering time. The generation testing across locations, years, and testers were conducted in Jeju Island (2008), Ansong (2009), and Kunwi Farm year-round. We developed 40 crosses of Silage 1 and 66 crosses of Silage 2 during winter season in KNUGH, 2007. Another two sets (19 crosses of 69B x P45 and 41 crosses of 51B x P45) were done at KNU Farm in Kunwi in 2008. The first crosses were planted with 2 checks (Suwon 19 and P3275) on April 16<sup>th</sup>, 2008 at Je-Dong Farm in Jeju Island. The second crosses were planted with 7 most Korean commercial hybrid (Suwon 19, Kangda Ok, Kwang Pyeong Ok, Jangda Ok and Cheong An Ok) from the Rural Development Administration (RDA) in Korea and 2 USA's commercial hybrids (P3257 and DK729) at Kunwi Farm on June 3<sup>rd</sup>, 2009. Field trials were designed in 2 m length in Jeju and 1 m length in Kunwi, 75 cm wide row with RCBD with three replications. Seeds were planted in 25 cm between hills with 2 seeds per hill. Fertilizer applications were at the rate of 200, 150, and 150 kg per hectare for N, P<sub>2</sub>O<sub>5</sub>, and K<sub>2</sub>O, respectively.

The infection of the disease was observed after mid-silking. Southern rust tolerance ratings were made on determining tolerance based on a 1 to 9 rating score, similar score rating used for *Puccinia Sorghi* Schw. and Downy mildew (DM) (Ajala et al. 2003, Kim et al. 1974 & 2003). Similarly to other diseases rating, which the rating scores has negative value with 1 = highly tolerant and 9 = highly susceptible. The investigations were done toward the important agronomic traits such as plant height (PH), ear height (EH), commercial value (Com.V.), and Southern rust infection. Data analysis was done with Statistical Analysis Software (SAS 9.1), 2005, GLM program.

## Results

### 1. Experiment I: 40 genotypes of Silage 1 (69B x P45) and 2 checks tested for Southern rust tolerance in Jeju (2008).

The analysis of variance showed:

- 1.1. Highly significant ( $P=0.001$ ) different for tolerance to Southern rust: Genotypes with Entry No. J1-2 (1002 (69B) x 1053 (P45) and J1-32 (1011 (69B) x 1043 (P45) were highly significant for tolerance followed by Entry No. J1-18 (1005 (69B) x 1052 (P45)), J1-40 (1013 (69B) x 1053 (P45)) and J1-41 (1015 (69B) x 1029 (P45)) (**Table 1**). Genotypes with Entry No. J1-30 (1009 (69B) x 1086 (P45)), J1-58 (P3275), J1-37 (1012 (69B) X 1044 (P45)), J1-33 (1011 (69B) x 1044 (P45) and J1-7 (1003 (69B) x 1085 (P45)) were susceptible for Southern rust infection from the  $Mean = 4.7$ ,  $CV = 22.9$  and  $LSD = 1.7$ .

1.2. Highly significant ( $P=0.001$ ) different for both EL and KRL. Genotypes with Entry No. J1-40 (1013 (69B) x 1053 (P45)) was the longest EL from the  $Mean=218.0$  mm,  $CV=6.3$  and  $LSD=22.3$  with 88% KRL from the  $Mean=90.8\%$  (Table 1). Entry No. J1-32 (1011 (69B) x 1043 (P45)) was the second longest EL with longest KRL with 94 % KRL from the  $Mean=197.0$ ,  $CV=7.7$  and  $LSD=24.0$ . The third longest EL

and second longest KRL was J1-19 (1005 (69B) x 1057 (P45)) with 94 % KRL. The analysis of variance for ED also showed highly significant ( $P=0.001$ ) different. Genotypes with Entry No. J1-55 (1064 (69B) x 1349 (P45)), J1-30 (1009 (69B) x 1086 (P45)), J1-47 (1021 (69B) x 1052 (P45)), J1-29 (1009 (69B) x 1051 (P45)) and J1-2 (1002 (69B) x 1053 (P45)) exhibited with biggest rate for ED from the  $Mean=45.5$ ,  $CV=8.5$  and  $LSD=6.3$ .

Table 1. Data of the important agronomic characters of 40 genotypes of Silage 1 and 2 checks at Je-Dong Farm in Jeju Island, 2008.

Pedigree	Entry	PH (cm)	EH (cm)	Com.V (1-9)	SrRt
1002 (69B) x 1029 (P45)	J1-1	244d-m	99c-h	5.3b-g	5.0b-e
1002 (69B) x 1053 (P45)	J1-2	252a-j	99c-h	4.7d-g	3.3e
1003 (69B) x 1030 (P45)	J1-3	297k-o	79i-k	5.0c-g	5.3a-d
1003 (69B) x 1029 (P45)	J1-4	201p	80i-k	6.0a-e	5.7a-c
1003 (69B) x 1052 (P45)	J1-5	232j-n	88g-j	5.7a-f	4.3c-e
1003 (69B) x 1032 (P45)	J1-6	219n-p	89f-j	4.7d-g	5b-e
1003 (69B) x 1085 (P45)	J1-7	209op	67k	6.7a-c	6.0ab
1004 (69B) x 1028 (P45)	J1-8	227l-o	87h-j	4.7d-g	4c-d
1004 (69B) x 1032 (P45)	J1-10	235h-n	89f-j	4.0f-g	4c-d
1004 (69B) x 1085 (P45)	J1-11	242d-m	102a-h	4.3e-g	5.3a-d
1005 (69B) x 1015 (P45)	J1-12	238f-n	105a-h	7.3a	5.3a-d
1005 (69B) x 1029 (P45)	J1-13	238f-n	92d-j	7.0ab	4.7b-e
1005 (69B) X 1031 (P45)	J1-14	243d-m	105a-h	5.3b-g	5b-e
1005 (69B) X 1032 (P45)	J1-15	242d-m	106a-g	5.0c-g	4.7b-e
1005 (69B) x 1052 (P45)	J1-18	254a-j	95c-i	4.0f-g	3.7de
1005 (69B) x 1057 (P45)	J1-19	244d-m	91e-j	4.7d-g	4.3c-e
1008 (69B) x 1053 (P45)	J1-23	263a-d	110a-c	4.3e-g	4.0c-d
1007 (69B) x 1051 (P45)	J1-24	256a-i	97c-i	4.7d-g	4.3c-e
1007 (69B) x 1052 (P45)	J1-25	252a-j	92c-j	4.7d-g	4.3c-e
1007 (69B) x 1053 (P45)	J1-26	256a-i	107a-f	4.3e-g	4.0c-d
1008 (69B) x 1051 (P45)	J1-27	256a-h	94c-j	5.7a-f	5.0b-e
1009 (69B) x 1051 (P45)	J1-29	233i-n	103a-h	3.7g	4.0c-d
1009 (69B) x 1086 (P45)	J1-30	246c-m	101b-h	6.0a-e	7.0a
1011 (69B) x 1032 (P45)	J1-31	249b-l	106a-f	4.3e-g	4.0c-d
1011 (69B) x 1043 (P45)	J1-32	272a	118ab	3.7g	3.3e
1011 (69B) x 1044 (P45)	J1-33	223m-p	110a-c	5.3b-g	6.0ab
1011 (69B) x 1041 (P45)	J1-34	259a-g	110a-d	4fg	4.7b-e
1011 (69B) x 1061 (P45)	J1-36	257a-h	108a-e	5.3b-g	4.0c-d
1012 (69B) X 1044 (P45)	J1-37	261a-f	108a-d	6.0a-e	6.0ab
1013 (69B) x 1053 (P45)	J1-40	271ab	119a	4.0fg	3.7de
1015 (69B) x 1029 (P45)	J1-41	268a-c	103a-h	3.7g	3.7de
1015 (69B) x 1030 (P45)	J1-42	256a-i	91e-j	4.3e-g	4.0c-d
1016 (69B) x 1029 (P45)	J1-43	262a-d	103a-h	4.3e-g	4.0c-d
1017 (69B) x 1029 (P45)	J1-46	261a-e	92d-j	4.3e-g	4.7b-e
1021 (69B) x 1052 (P45)	J1-47	261a-f	102a-h	4fg	4.0c-d
1025 (69B) x 1052 (P45)	J1-49	253a-j	104a-h	3.7g	3.7ed
1026 (69B) x 1052 (P45)	J1-51	238f-n	98c-h	4.7d-g	5.0b-e
1041 (P45) x 1007 (69B)	J1-54	257a-h	109a-e	5c-g	5.3a-d
1064 (69B) x 1349 (P45)	J1-55	251a-k	106a-f	4.3e-g	5.3a-d
1071 (69B) x 1351 (P45)	J1-56	252a-j	102a-h	4.3e-g	5.3a-d
S19	J1-57	237g-n	77jk	6.3a-d	5.7a-c
32P75	J1-58	228lk-o	80i-k	5.7a-f	6.0ab
Mean		246	98.2	4.9	4.7
Coefficient of variance (CV)		5.73	11.32	23.46	1.07
LSD		22.87	18.04	1.86	1.74

Rust rating scores (1 – 9): 1= highly tolerant, 9= highly susceptible.



Figure 1.A. Southern rust infection on *sh* trials at Kunwi Farm (2006). Fig. 1.B. Southern rust tolerant lines in Jeju (2008). Fig. 1.C. Breeding for Southern rust tolerant at Kunwi Farm in 2009 (left: tolerant line; right: susceptible line). Fig. 1.D. Yield trial of Silage 2 and commercial cultivars in Ansong (2009).

1.3. Highly significant ( $P=0.006$ ) different for Com.V. from the  $Mean= 4.88$ ,  $CV= 23.46$  and  $LSD= 1.86$ . Genotypes with Entry No. J1-29 (1009 (69B) x 1051 (P45)), J1-32 (1011 (69B) x 1043 (P45)), J1-41 (1015 (69B) x 1029 (P45)) and J1-49 (1025 (69B) x 1052 (P45)) showed the highest rate for mean of the important agronomic traits (Table 1). The results also showed highly positive correlation ( $y= 1.565 + 0.708x$ ;  $r^2= 0.433$ ) between Southern rust infection and Com.V. (Figure 2). Genotypes with low infection showed good performance for the mean value of the important agronomic traits.

**2. Experiment II: 41 genotypes of Silage 2 (51B x P45) and 2 checks tested for Southern rust tolerance in Jeju (2008).**

The analysis of variance showed:

2.1. Highly significant ( $P=0.001$ ) different for Southern rust tolerance. Genotypes with Entry No. J2-13 (1034(P45) x 1206(51B)), J2-15 (1034(51B) x 1224(51B)), J2-16 (1034(P45) x 1227(51B)), J2-31 (1038(P45) x 1227(51B)) and J2-56 (1057(P45) x 1206(51B)) exhibited the highest rate for tolerance to Southern rust

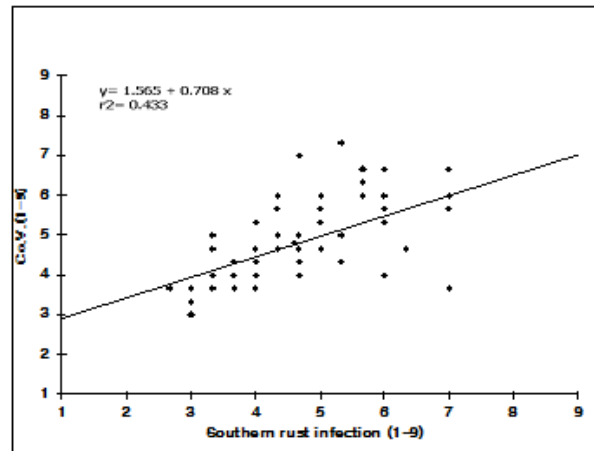


Figure 2. Correlation between Southern rust infection and commercial value of 40 genotypes and 2 checks tested in Jeju, 2008.

infection from the  $Mean= 4.1$ ,  $CV= 20.8$  and  $1.4$  (Table 2). The highly susceptible genotypes were Cheong An Ok, Jangda Ok, Kangda Ok and J2-41 (1221(51B) x 1043(P45)).

Table 2. Agronomic characters of 65 selected crosses of Silage 2 tested at Je-Dong Farm, Jeju Island, 2008.

Pedigree	Entry No.	PH (cm)	EH (cm)	Com.V (1-9)	SrRt
1218(51B) x 1028(P45)	J2-1	255a-i	80l-n	4.3d-h	3.7f-i
1029(P45) x 1225 (51B)	J2-2	273a	133a-c	4.3d-h	3.7f-i
1030(P45) x 1205(51B)	J2-3	250b-l	105d-l	4.0e-i	3.3g-i
1004 (69B) x 1031(P45)	J2-4	238h-o	95f-n	5.3b-e	4.3d-h
1031(P45) x 1205(51B)	J2-5	260a-f	123a-e	3.6f-i	3.3g-i
1209(51B) x 1032(P45)	J2-6	230l-o	88i-n	5.7a-d	4.3d-h
1212(51B) x 1032(P45)	J2-7	250b-l	90h-n	4.0e-i	4.3d-h
1213(51B) x 1032(P45)	J2-8	233k-o	83k-n	5.3b-e	5.0c-f
1224(51B) x 1032(P45)	J2-9	238h-o	85j-n	5.0c-f	5.0c-f
1033(P45) x 1205 (51B)	J2-10	238h-o	100e-m	4.0e-i	3.3g-i
1033(P45) x 1206 (51B)	J2-11	255a-i	118a-f	3.3g-i	3.0hi
1034(P45) x 1205(51B)	J2-12	238h-o	103d-m	5.0c-f	3.3g-i
1034(P45) x 1206(51B)	J2-13	270ab	133a-c	3.3g-i	2.7i
1034(51B) x 1214(51B)	J2-14	252b-j	100e-m	4.0e-i	3.0hi
1034(51B) x 1224(51B)	J2-15	255a-i	113a-h	3.3g-i	2.7i
1034(P45) x 1227(51B)	J2-16	253a-j	115a-h	3.3g-i	2.7i
1035(P45) x 1205(51B)	J2-17	230l-o	87i-n	5.0c-f	4.0e-i
1035(P45) x 1206(51B)	J2-18	234j-o	92g-n	5.0c-f	3.0hi
1210(51B) x 1035(P45)	J2-19	258a-g	73n	4.0e-i	4.0e-i
1035(P45) x 1245(51B)	J2-20	245d-m	93f-n	4.0e-i	4.0e-i
1036(P45) x 1206(51B)	J2-21	252b-j	113a-h	3.3g-i	3.3g-i
1036(P45) x 1223(51B)	J2-22	243d-m	97f-n	3.3g-i	5.0c-f
1036(P45) x 1225(51B)	J2-23	260a-f	110b-j	3.0hi	3.0hi
1037(P45) x 1223(51B)	J2-25	242e-n	92g-n	4.3d-h	3.3g-i
1038(P45) x 1204(51B)	J2-27	225m-o	102d-m	5.0c-f	3.3g-i
1038(P45) x 1206(51B)	J2-28	245d-m	108c-j	3.7f-i	3.7f-i
1038(P45) x 1206(51B)	J2-29	242e-n	103d-m	4.3d-h	3.3g-i
1038(P45) x1226(51B)	J2-30	262a-e	127a-d	3.7f-i	3.7f-i
1038(P45) x 1227(51B)	J2-31	267a-c	135ab	2.7i	2.7i
1038(P45) x 1227(51B)	J2-32	258a-g	112b-i	3.7f-i	3.3g-i
1224(51B) x 1039(P45)	J2-33	235i-o	117a-g	6.7ab	6.0a-c
1041(P45) x 1205(51B)	J2-34	240f-n	107d-k	5.0c-f	3.0hi
1041(P45) x 1211(51B)	J2-35	240f-n	95f-n	4.7c-g	3.0hi
1041(P45) x 1223(51B)	J2-37	258 a-g	113a-h	4.3d-h	3.3g-i
1041(P45) x 1225(51B)	J2-38	252b-j	108c-j	4.0e-i	3.0hi
1225(51B) x 1041(P45)	J2-39	238g-o	78mn	4.7c-g	5.0c-f
1205(51B) x 1043(P45)	J2-40	252b-j	97f-n	5.7a-d	4.3d-h
1221(51B) x 1043(P45)	J2-41	222no	92g-n	7.0a	7.0a
1210(51B) x 1050(P45)	J2-42	233j-o	92g-n	4.3d-h	5.0c-f
1203(51B) x 1051(P45)	J2-43	262a-e	102d-m	4.0e-i	5.3b-e
1219(51B) x 1051(P45)	J2-44	240f-n	80l-n	3.7f-i	3.7f-i
1220(51B) x1051(P45)	J2-45	235i-o	80l-n	5.0c-f	3.7f-i
1223(51B) x 1051(P45)	J2-47	253a-j	93f-n	5.0c-f	4.3d-h
1223(51B) x 1051-53(P45)	J2-48	245d-m	85j-n	4.0e-i	3.3g-i
1225(51B) x 1051(P45)	J2-49	258a-g	108c-j	4.3d-h	3.7f-i
1227(51B) x 1051(P45)	J2-50	227m-o	102d-m	4.3d-h	4.0e-i
1223(51B) x 1052(P45)	J2-51	244d-m	78mn	3.7f-i	4.0e-i
1125(51B) x 1051(P45)	J2-52	237h-o	87i-n	3.3g-i	3.0hi
1210(51B) x 1053(P45)	J2-54	262a-e	98e-n	3.3g-i	3.0hi
1224(51B) x 1053(P45)	J2-55	243d-m	97f-n	4.7c-g	4.0e-i
1057(P45) x 1206(51B)	J2-56	248c-l	112b-i	3.7f-i	2.7i
1057(P45) x 1206(51B)	J2-57	255a-i	110b-j	5.0c-f	3.3g-i
1060(P45) x 1226(51B)	J2-59	253a-j	118a-f	3.0hi	3.0hi
1061(P45) x 1203(51B)	J2-60	252b-j	102d-m	4.7c-g	4.7c-g
1225(51B) x1061(P45)	J2-61	263a-d	107d-k	3.7f-i	3.0hi
1062(P45) x 1203(51B)	J2-62	233j-o	90h-n	6.0a-c	4.3d-h
1062(P45) x 1206(51B)	J2-63	232k-o	97f-n	5.3b-e	4.0e-i
1062(P45) x 1209(51B)	J2-64	222no	82k-n	6.7ab	5.7a-d
1223(51B) x 1062(P45)	J2-65	238g-o	87i-n	6.0a-c	5c-f
P3257	P3257	252b-j	105d-l	4.7c-g	6.3ab
DK729	DK729	260a-f	117a-g	4.7c-g	6.3ab
P3394	P3394	243d-m	85j-n	5.3b-e	6.0a-c

Table 2. Continued.

Pedigree	Entry No.	PH (cm)	EH (cm)	Com.V (1-9)	SrRt
Kangda Ok		245d-m	110b-j	3.7f-i	7.0a
Kwang Pyong Ok		257a-h	92g-n	4.0e-i	6.0a-c
Jangda Ok		245d-m	138a	6.7ab	7.0a
Cheong An Ok		218o	82k-n	5.7a-d	7.0a
Mean		246.1	100.7	4.4	4.1
CV		5.04	15.7	23.16	20.84
LSD		20.02	25.64	1.66	1.38
		***	***	***	***

SrRt= Southern rust

Rust rating scores (1 – 9): 1= highly tolerant, 9= highly susceptible.

2.2. Highly significant ( $P=0.001$ ) different for Com.V. Genotypes with Entry No. J2-31 (1038(P45) x 1227(51B)), J2-59 (1060(P45) x 1226(51B)) and J2-23 (1036(P45) x 1225(51B)) showed highest Com.V. from the  $Mean= 4.4$  ( $CV=23.2$  and  $LSD= 1.7$ ) (Table 2). Meanwhile, the analysis of variance showed highly positive correlation ( $y= 2.468 + 0.483x$ ;  $r^2= 0.358$ ) between Southern rust infection and Com.V. (Figure 3). Plants with high infection exhibited pustules on the leaves and sheaths causing leaf damage that eventually causing yield lost. The criterion used for Com.V. was the mean of the important agronomic traits related to yield.

**3. Experiment III: 19 genotypes of Silage 1 (69B x P45) and 7 checks tested for Southern rust tolerance at Kunwi Farm (2009)**

The analysis of variance showed:

- 3.1. Significant different ( $P=0.041$ ) for Southern rust infection from the  $Mean= 4.3$ ,  $CV= 23.9$  and  $LSD= 1.67$ . Genotypes with the highest rates for tolerance were J1-7 (69B-2 x P45-79), J1-9 (69B-3 x P45-9), J1-8 (69B-3 x P45-1), J1-11 (69B-3 x P45-20), and J1-12 (69B-3 x P45-46) (Table 3). Susceptible genotypes were Ch-7 (Swon-19), Ch-2 (Kwang Pyeong Ok), Ch-5 (Cheong an Ok) and J1-13 (69B-3 x P45-81).
- 3.2. Highly significant ( $P=0.004$ ) different for Com.V. Genotypes with the highest rates for Com.V. were Entry No. J1-31 (69B-6 x P45-24), J1-7 (69B-2 x P45-79) and J1-10 (69B-3 x P45-14) (Table 3). Genotypes with the lowest rates for Com.V. were Ch-7 (Suwon 19) and other 10 genotypes. Meanwhile, the analysis of variance showed positive correlation ( $y= 2.337 + 0.372x$ ;  $r^2= 0.202$ ) between Southern rust infection and Com.V. (Figure 4). The result revealed that genotypes with high infection showed poor commercial value.

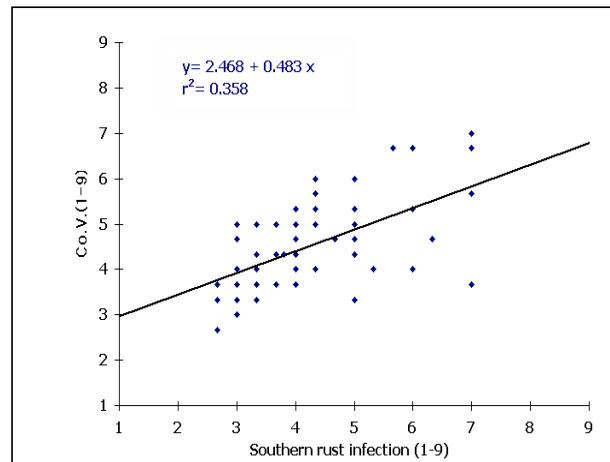


Figure 3. Correlation of Southern rust and Commercial value of 59 genotypes of Silage 2 and 7 checks tested in Jeju, 2008.

**4. Experiment IV: 41 genotypes of Silage 2 (51B x P45) and 7 checks tested for Southern rust tolerance at Kunwi Farm (2009)**

The analysis of variance showed:

- 4.1. Highly significant ( $P=0.001$ ) different for Southern rust infection from the  $Mean= 4.2$  ( $CV= 22.5$  and  $LSD 1.5$ ). The highest rates were genotypes with Entry No. J2-1 (51B-2 x P45-11), J2-6 (51B-2 x P45-22), J2-12 (51B-3 x P45-26), J2-69 (51B-29 x P45-8) and J2-25 (51B-48 x P45-95) (Table 4) for tolerance to Southern rust infection from the  $Mean= 4.2$  ( $CV= 22.5$  and  $LSD= 1.5$ ). The lowest rates were genotypes with Entry No. J3-11 (51B-39 x P45-7), Ch-7 (Swon-19), Ch-5 (Cheong an Ok), Ch-2 (Kwang Pyeong Ok) and J3-29 (51B-48 x P45-13) for susceptible. There was no any plant escaped from the infection.
- 4.2. Highly significant ( $P=0.001$ ) different for Com.V. Genotypes with the highest rates for Com.V. were

Table 3. Data of the important agronomic characters of 26 genotypes of Silage 1 at Kunwi Farm, 2009.

Pedigree	Entry No	PH (cm)	EH (cm)	StRst (1-9)	Com.V..
69B-2 x P45-44	J1-3	268a-e	102	4.3a-c	3.3c-e
69B-2 x P45-90	J1-4	293a	110	4.0a-c	4.0b-d
69B-2 x P45-20	J1-5	250c-f	137	4.0a-c	4.3bc
69B-2 x P45-47	J1-6	292ab	140	4.7a-c	4.0b-d
69B-2 x P45-79	J1-7	292ab	127	3.3c	3.0de
69B-3 x P45-1	J1-8	267a-e	113	3.7bc	3.7b-e
69B-3 x P45-9	J1-9	262a-e	108	3.3c	4.0b-d
69B-3 x P45-14	J1-10	279a-d	120	4.0a-c	3.0de
69B-3 x P45-20	J1-11	262a-e	115	3.7bc	3.3c-e
69B-3 x P45-46	J1-12	263a-e	110	3.7bc	4.0b-d
69B-3 x P45-81	J1-13	248d-f	107	5.7a	4.3bc
69B-3 x P45-99	J1-14	262a-e	120	5.0a-c	3.7b-e
69B-3 x P45-107	J1-15	255c-e	128	3.7bc	4.0b-d
69B-3 x P45-109	J1-16	258c-e	107	4.0a-c	4.0b-d
69B-4 x P45-1	J1-17	267a-e	78	4.3a-c	4.0b-d
69B-4 x P45-14	J1-19	278a-e	130	3.7bc	4.7b
69B-4 x P45-20	J1-20	282a-c	128	3.7bc	3.7b-e
69B(?) -6 x P45-24	J1-31	255c-e	105	3.7bc	2.7e
69B-7 x P45-110	J1-36	260b-e	102	3.7bc	4.0b-d
Kangda Ok -check-1	Ch-1	255c-e	120	5a-c	3.3c-e
Kwang Pyong Ok - check-2	Ch-2	247e-f	90	5.7a	4.3bc
Janda Ok-check-3	Ch-3	265a-e	95	5.3ab	4.7b
Cheong sa Ok-check-4	Ch-4	250c-f	112	4.3a-c	4.0b-d
Cheon an Ok-check-5	Ch-5	222f	95	5.7a	4.0b-d
P3394-check-6	Ch-6	248d-f	108	3.7bc	4.3bc
Swon-19-check-7	Ch-7	257c-e	105	5.7a	6.0a
Mean		262.9	112.0	4.4	3.9
CV		7.51	18.86	23.85	18.49
LSD		32.4	34.63	1.68	1.19
		*	ns	*	**

SrRt= Southern rust

Rust rating scores (1 – 9): 1= highly tolerant, 9= highly susceptible.

Entry No. J3-3 (51B-36 x P45-7), J2-1 (51B-2 x P45-11), J3-7 (51B-37 x P45-2), J3-5 (51B-36 x P45-46), J2-75 (51B-29 x P45-82), J2-74 (51B-29 x P45-46), J2-69 (51B-29 x P45-8), J2-12 (51B-3 x P45-26) and J2-5 (51B-3 x P45-26) (Table 4) for good performance for important agronomic traits from the *Mean*= 3.76, *CV*=18.75 and *LSD*= 1.13. Genotypes with lowest Com.V. were J3-29 (51B-48 x P45-13), Ch-7 (Suwon-19), J2-77 (51B-30 x P45-4), J3-11 51B-39 x P45-7) and Ch-3 (Jangda Ok). Meanwhile, the analysis of variance showed highly positive correlation ( $y = 1.596 + 0.517x$ ;  $r^2 = 0.371$ ) between Southern rust infection and Com.V. (Figure 5). The result with highly positive correlation revealed the importance of breeding for tolerant cultivars.

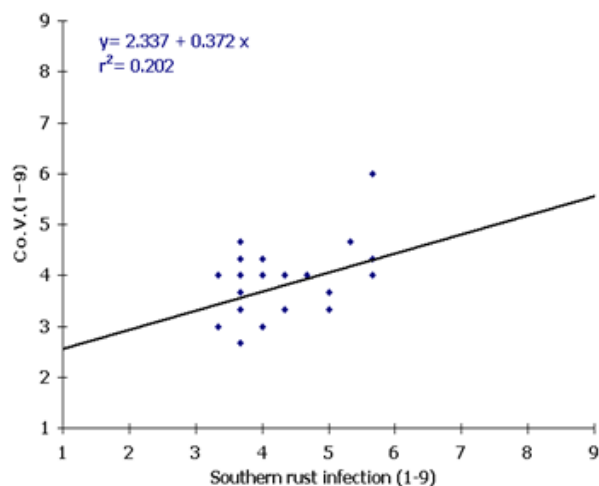


Figure 4. Correlation of Southern rust infection and Co.V. of 19 genotypes of Silage 1 and 7 checks of commercial cultivars and hybrids from the RDA and USA respectively, tested in Kunwi, 2009.

Table 4. Data of the important agronomic characters of Silage 2 at Kunwi Farm, 2009.

Pedigree	Entry No	PH (cm)	EH (cm)	Com.V. (1-9)	StRst (1-9)
51B-2 x P45-11	J2-1	273a-j	132a-g	2.7e	3.0f
51B-2 x P45-13	J2-2	260c-l	113c-k	3.3d-f	3.3ef
51B-2 x P45-22	J2-3	295a-e	108d-k	3.7c-f	3.3ef
51B-2 x P45-110	J2-4	248h-l	112d-k	3.7c-f	3.7d-f
51B-3 x P45-26	J2-5	273a-j	100h-k	3.0ef	3.3ef
51B-2 x P45-22	J2-6	295a-e	125a-i	3.3d-f	3.0f
51B-3 x P45-22	J2-11	263c-j	100h-k	3.7c-f	3.7d-f
51B-3 x P45-26	J2-12	277a-j	113c-k	3.0ef	3.0f
51B-12 x P45-1	J2-27	277a-j	123a-j	3.3d-f	4.0c-f
51B-13 x P45-11	J2-29	257d-l	102g-k	3.7c-f	4.0c-f
51B-43 x P45-4	J2-32	283a-i	123a-j	3.3d-f	5.3a-c
51B-26 x P45-82	J2-66	270a-j	117b-k	3.7c-f	4.3b-f
5B-27 x P45-9	J2-67	247i-l	100h-k	3.7c-f	3.3ef
51B-35 x P45-9	J2-68	238j-l	93j-k	4.0b-e	5.0a-d
51B-29 x P45-8	J2-69	273a-j	115c-k	3.0ef	3.0f
51B-29 x P45-21	J2-71	292a-f	118b-k	4.0b-e	3.3ef
51B-29 x P45-21	J2-72	308a	152a	3.3d-f	3.7d-f
51B-29 x P45-45	J2-73	300a-c	128a-h	3.3d-f	4.0c-f
51B-29 x P45-46	J2-74	305ab	135a-e	3.0ef	4.0c-f
51B-29 x P45-82	J2-75	288a-h	143a-c	3.0ef	4.0c-f
51B-30 x P45-18	J2-76	270a-j	138a-d	3.3d-f	4.0c-f
51B-30 x P45-4	J2-77	262c-k	122a-j	5.0ab	5.0a-d
51B-30 x P45-82	J2-78	292a-f	132a-g	3.7c-f	3.7d-f
51B-30 x P45-9	J2-79	262c-k	117b-k	4.3b-d	4.7a-e
51B-30 x P45-21	J2-80	290a-g	120b-k	3.7c-f	3.7d-f
51B-35 x P45-82	J3-2	265b-j	105e-k	4.3b-d	5.0a-d
51B-36 x P45-7	J3-3	297a-d	133a-f	2.7e	3.7d-f
51B-36 x P45-13	J3-4	270a-j	132a-g	4.0b-e	4.0c-f
51B-36 x P45-46	J3-5	300a-c	133a-f	3.0ef	4.7a-e
51B-36 x P45-79	J3-6	278a-j	118b-k	3.7c-f	4.0c-f
51B-37 x P45-2	J3-7	285a-i	123a-j	3.0ef	5.0a-d
51B-37 x P45-9	J3-8	262c-k	100h-k	3.7c-f	5.0a-d
51B-39 x P45-7	J3-11	272a-j	115c-k	5.0ab	6.0a
51B-39 x P45-21	J3-12	253f-l	100h-k	4.0b-e	3.7d-f
51B-41 x P45-2	J2-13	257d-l	107e-k	4.3b-d	4.0c-f
51B-44 x P45-23	J3-16	305ab	147ab	3.7c-f	3.3ef
51B-44 x P45-23	J3-17	258d-l	103e-k	3.3d-f	4.0c-f
51B-45 x P45-4	J3-18	258d-l	108d-k	4.3b-d	5.0a-d
51B-48 x P45-95	J2-25	252f-l	107e-k	3.3d-f	3.0f
51B-48 x P45-5	J3-28	265b-j	118b-k	4.0b-e	3.6d-f
51B-48 x P45-13	J3-29	220l	108d-k	6.0a	5.7ab
Kangda Ok	Ch-1	255e-l	120b-k	3.3d-f	5.0a-d
Kwang Pyong Ok	Ch-2	247i-l	90k	4.3b-d	5.6ab
Janda Ok	Ch-3	265b-j	95i-k	4.7bc	5.3a-c
Cheong sa Ok	Ch-4	250g-l	112d-k	4.0b-e	4.3b-f
Cheon an Ok	Ch-5	222kl	95i-k	4.0b-e	5.7ab
P3394	Ch-6	248h-l	108d-k	4.3b-d	3.7d-f
Swon-19	Ch-7	257d-l	105e-k	6.0a	5.7ab
Mean		269.6	115.9	3.8	4.2
CV		9.39	16.82	18.57	22.46
LSD (0.05)		41.01	31.61	1.13	1.52
		**	*	***	***
Probability		0.002	0.02	0.001	0.001

SrRt= Southern rust

Rust rating scores (1 – 9): 1= highly tolerant, 9= highly susceptible.

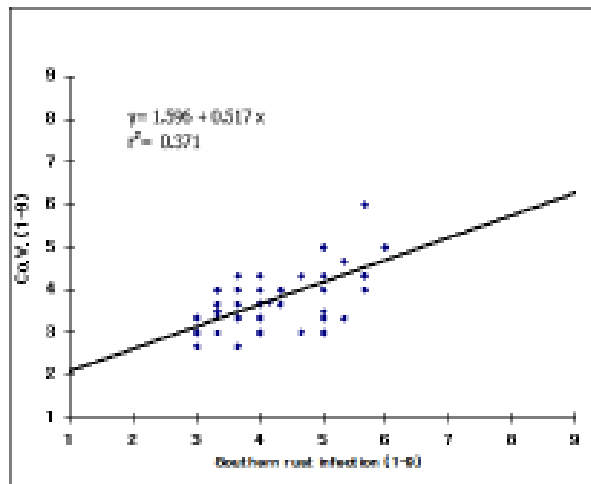


Figure 5. Correlation between Southern rust infection and Co.V. of 41 genotypes of Silage 2 and 7 checks of commercial cultivars and hybrids from RDA and USA respectively, tested in Kunwi, 2009.

## DISCUSSION

### Southern Rust Infection

Genotypes of Silage 1, Silage 2 and 7 checks of commercial cultivars from the RDA and USA showed highly significant different for Southern rust infection in Jeju Island and at Kunwi Farm. However, all genotypes showed no escaped plant from the disease infections. Host plants exhibited different responses from the level of tolerance to highly susceptible. During our breeding process by year-round, we have developed promising lines with tolerance to Southern rust and good yield potential. Tolerant plants with a little infection were quickly recovered with producing high yield. Our experiences revealed that single gene controlled high resistance cannot be durable. The possibility is to breed host tolerance with polygenic system with a threshold nature. Parlevliet and Zadoks (1977) reported that polygenic resistance operating on a gene-for-gene basis with polygenes in the pathogen could be race non-specific or horizontal in nature. Controlling pest through tolerance can only permit co-survive of pest and host with durable and environmentally-friendly (Kim 2000). Sleper *et al.* (2006) reported that new crosses should be tested in multi-seasons and multi-environment to fix that the superior lines in a population are due to genetic potential, favorable environment, or both positive genetic x environment interaction.

The mean of Southern rust infection of Silage 1 and Silage 2 at two locations in Jeju Island and Kunwi showed

varied. The highest mean rate was Silage 2 with 4.1 and 4.2 in Jeju and at Kunwi Farm, respectively. Genotypes with the highest tolerance rates were 2.7 with Entry No. J2-16 (1034(P45) x 1227(51B)), J2-31 (1038(P45) x 1227(51B)) and J2-56 (1057(P45) x 1206(51B) in Jeju Island and 3.0 for Entry No. J2-1 (51B-2 x P45-11), J2-8 (51B-3 x P45-26), J2-15 (51B-29 x P45-8) and J2-39 (51B-48 x P45-95) at Kunwi Farm. Meanwhile, Mean rates of Silage 1 were 4.7 and 4.3 in Jeju Island and at Kunwi Farm, respectively. The genotypes were Entry No. J1-2 (1002 (69B) x 1053 (P45)) and J1-32 (1011 (69B) x 1043 (P45)) with highest rates 3.3 in Jeju Island and Entry No. J1-7 (69B-2 x P45-79) and J1-9 (69B-3 x P45-9) and 3.3 at Kunwi Farm.

### Ear Length, Kernel Row Length and Ear Diameter

The importances of yield components were EL, KRL, ED and kernel depth. Plant with long EL and KRL, big ED and depth kernels produce high yield. However, our breeding experiences showed that genotypes with those traits were most genotypes with long days to silking and high EH. **Mendoza (1979)** stated that selection response for increased ear length was not accompanied by a correlated response in grain yield per plant and selection response for decreased ear length, however, was accompanied by a significant response for decreased grain yield per plant. The result of our experiments showed no any genotype among Silage 1 and Silage 2 had highest rates for the three traits. However, Silage 1 (J1) with Entry No. J1-32 (1011 (69B) x 1043 (P45)), J1-40 (1013 (69B) x 1053 (P45)) and J1-19 (1005 (69B) x 1057 (P45)) were confirmed to have highest rates for EL and KRL and also Southern rust. The KRL percentages (%) were 94 %, 88.0 % and 93.7 %, respectively. Meanwhile, 5 genotypes of Silage 2 (J2) trial with highest rate for EL showed that only Entry No. J2-54 (1210(51B) x 1053(P45)) and J2-19 (1210(51B) x 1035(P45)) exhibited highest rates for KRL with length 266.7 mm and 249.3 mm, respectively from the Mean 197.0. The KRL percentage (%) were 88.4 and 91.2, respectively with the highest rates for Commercial value.

### Correlations between Southern Rust Infection, Commercial Value, Ear Length and Ear Diameter

The correlated response of Southern rust and Com.V. was varied from low to highly positive correlation. Four sets of silage trials at different environments showed highly positive correlation for three trials. Genotypes with highly infected exhibited poor for Com.V. with low dry matter and

low grain yield. Silage 1 trial at Kunwi Farm exhibited significant differences at 3.3 and 5.7 for minimum and maximum, respectively. Meanwhile, ear length and ear diameter for both Silage 1 and Silage 2 were slightly positive correlation. Our breeding experiences showed that selection for increasing ear length was not accompanied by a correlated response in grain yield per plant. It revealed that grain yield was correlated with other traits such as ED and kernel depth. The correlated responses of grain yield per plant, ear diameter, kernel depth, ear height, and days to silking also were asymmetrical (Cortez-Mendoza et al. (1979). In Jeju, trials of Silage 1 and Silage 2 showed varied in low correlation with  $y = 24.831 + 0.095 x$  and very low correlation with  $y = 44.948 + 0.011 x$ , respectively for the correlation between EL and ED. Figures showed that ears with highest rate for EL had only medium size for ED. Ear length (EL) and ear diameter (ED) are two of the most important yield components related to yield and plant morphology (Zhang et al., 2010).

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